

Appendix III

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23°C during daylight hours (15h) and dropped to 15°C at night. Foliage blight scores were recorded 69, 92, 116, and 163 hours after inoculation. A blight scale, with 0 indicating a dead plant and 9 no visible infection, was used to visually rate disease severity. All the plants were tested in three repetitions. The ratings and the ranges of percentage infections associated with the rating value were as follows: 9, no visible infection; 8, less than 10% infection; 7, 11-25% infection; 6, 26-40% infection; 5, 41 to 60% infection; 4, 61-70% infection; 3, 71-80% infection; 2, 81-90% infection; 1, greater than 90% infection; 0, all dead. Plants with scores of 8 or above were scored as resistant and plants with scores of 6.9 or below were scored as susceptible. Plants with scores between 6.9 and 8 were scored as intermediate resistant.

Transgenic plants with gene 2 were tested using the above method. 69, 92, 116, and 163 hours after inoculation, the average resistant score for transgenic plants with gene 2 was 7.3.

Example 5:

The following example shows an amino acid comparison between the gene 2 coding region from a disease resistant and disease susceptible variety. The top sequence is the gene 2 coding region from the susceptible 177013 homolog. The bottom sequence is the gene 2 coding region from the resistant homolog. Note that on the line numbered 451, at residue 454, a single nucleotide difference between R and S changes a Tyrosine (Y; resistant) to an amber stop codon.

20		1 MAEAFTQVLLDNLTSFLKGELALLFGFQDEFQRLLSMFSTIQAVLEDAQE 50
		1 MAEAFTQVLLDNLTSFLKGELVLFGFQDEFQRLLSMFSTIQAVLEDAQE 50
25		S1 KQLNNKPLENWLOQLNAAATYEVDDILDEYKTRATPFSQSEYGRYHPKVIP 100
		S1 KQLNNKPLENWLOQLNAAATYEVDDILDEYKTRATPFSQSEYGRYHPKVIP 100
30		101 FRHKVGKRMQVMKKLKATAEERKNFHLMHEKIVERQAVRRETGSVLTEPQ 150
		101 FRHKVGKRMQVMKKLKATAEERKNFHLMHEKIVERQAVRRETGSVLTEPQ 150
		151 VYGRDKEKDEIVKILINNVSDAQHLSVLPILGMCGLGKTTLAQMVFNDQR 200
35		151 VYGRDKEKDEIVKILINNVSDAQHLSVLPILGMCGLGKTTLAQMVFNDQR 200
		201 VTERFHFSKIWICVSEDFDDEKRLIKAIIVESIEGRPLGEMDLAPLQQKKLQE 250
		201 VTERFHFSKIWICVSEDFDDEKRLIKAIIVESIEGRPLGEMDLAPLQQKKLQE 250
40		251 LLNGKRYLLVLDDVVNEQQKWNANLRAVLKVVGASGASVLTTRLEKGSI 300
		251 LLNGKRYLLVLDDVVNEQQKWNANLRAVLKVVGASGASVLTTRLEKGSI 300
45		301 MGTLQPYELSNSLQEDCWLIFMQRAGHQQEEINFNLVAIGKEIVKKSGGV 350
		301 MGTLQPYELSNSLQEDCWLIFMQRAGHQQEEINFNLVAIGKEIVKKSGGV 350

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Sequence Listing

351 PLAAKTLGGILCFKREERAWEHVRD SPIWNL PQDESSILP ALRLSYHQ LP 400
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351 PLAAKTLGGILCFKREERAWEHVRD SPIWNL PQDESSILP ALRLSYHQ LP 400
5 401 LOLKQCFAYCAVFPKDAKMKEKEKLISLWMAHGFLLSKGNNMELEDVGDEVW 450
||||| ||||| ||||| .||||| ||||| ||||| |||||
401 LOLKQCFAYCAVFPKDAKMKEKEKLISLWMAHGFLLSKGNNMELEDVGDEVW 450
10 451 KEL* LRSFFQ EIEVKDGKTYFKMHD LIDHLATSLFSANTSSSNIREINKH 500
||||| ||||| ||||| ||||| ||||| |||||
451 KELYLRSFFQ EIEVKDGKTYFKMHD LIDHLATSLFSANTSSSNIREINKH 500
15 501 SYTHMMMSICFAEVVFFFYTLIPPLEKFISLRVNLGDSTFNKL PSSIGDLVH 550
||||| ||||| ||||| ||||| ||||| |||||
501 SYTHMMMSICFAEVVFFFYTLIPPLEKFISLRVNLGDSTFNKL PSSIGDLVH 550
20 551 LRYLNLYGSGMRSLEPKQLCQLQNLQTLDLQYCTKLCCLPKETSKLGSLRN 600
||||| ||||| ||||| ||||| |||||
551 LRYLNLYGSGMRSLEPKQLCQLQNLQTLDLQYCTKLCCLPKETSKLGSLRN 600
601 LLIDGSQSLTCMPPRIGSLTCLTKLQQFVGRKKCYQLGELGNLNLYGSI 650
||||| ||||| ||||| ||||| |||||
601 LLIDGSQSLTCMPPRIGSLTCLTKLQQFVGRKKCYQLGELGNLNLYGSI 650
25 651 KISHLERVKNNDKDAKEANL SAKGNL HSLSMSWNNFGPHIYESEEVKVLEA 700
||||| ||||| ||||| ||||| |||||
651 KISHLERVKNNDMDOANEANL SAKGNL HSLSMSWNNFGPHIYESEEVKVLEA 700
30 701 LKPHSNLTSI KIYGF RGIHLPFW MNHS VLK NIVS I L ISNFRNC SCLE PFG 750
||||| ||||| ||||| ||||| |||||
701 LKPHSNLTSI KIYGF RGIHLPFW MNHS VLK NIVS I L ISNFRNC SCLE PFG 750
35 751 DLPCLESLELHWGSA DVEY VEEVDIDVHSGFPTRIRFPSLRKLDI WDFGS 800
||||| ||||| ||||| ||||| |||||
751 DLPCLESLELHWGSA DVEY VEEVDIDVHSGFPTRIRFPSLRKLDI WDFGS 800
801 LKGLLKKECEEQFPVLEEMTIHECPFLTLSSNLRALTSLRICYNKVATSF 850
||||| ||||| ||||| |||||
801 LKGLLKKECEEQFPVLEEMTIHECPFLTLSSNLRALTSLRICYNKVATSF 850
851 PEEMFKNLANLKYLTISRCNNL KELPTSLASLNALKSL ALES L P 894
||||| ||||| ||||| |||||
851 PEEMFKNLANLKYLTISRCNNL KELPTSLASLNALKSL KIQLCCALES L P 890
45 895 EEEGLEGLSSLTTEL FVEHCNMLNCLPEGLQHLLTSLKIRGC PQLIKRCE 944
||||| ||||| ||||| ||||| |||||
901 EEEGLEGLSSLTTEL FVEHCNMLKCLPEGLQHLLTSLKIRGC PQLIKRCE 950
50 945 KG1GEDWHRKISHIPNVNIYI* 965
||||| |||||
951 KG1GEDWHRKISHIPNVNIYI* 971

55 Example 6:

The following example shows a nucleic acid comparison between the gene 2 coding regions from a disease resistant and disease susceptible variety. The top sequence is the gene 2 coding region from the resistant homolog. The bottom sequence is the gene 2 coding region